

**SCORE Search Results Details for Application 10552515 and Search Result 20080624\_135830\_us-10-552-515-1\_copy\_157\_933.rup.**

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10552515 and Search Result 20080624\_135830\_us-10-552-515-1\_copy\_157\_933.rup.

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GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: June 24, 2008, 15:17:39 ; Search time 529 Seconds  
(without alignments)  
2416.325 Million cell updates/sec

Title: US-10-552-515-1\_COPY\_157\_933  
Perfect score: 4123  
Sequence: 1 QQDVQDGNTTVHYALLSASW.....SELSSHWTPFTVPKASQLQQ 777

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_12.1:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4123	100.0	933	1	TM16G_HUMAN	Q6iwh7 homo sapien
2	3478.5	84.4	859	1	TM16G_MOUSE	Q14at5 mus musculu

3	3472	84.2	860	1	TM16G_RAT	Q6ift6	rattus norv
4	1505.5	36.5	920	2	A6QLE6_BOVIN	A6qle6	bos taurus
5	1498.5	36.3	955	1	TM16D_HUMAN	Q32m45	homo sapien
6	1476.5	35.8	903	2	Q1AP36_STRPU	Q1ap36	strongyloce
7	1475.5	35.8	921	2	Q1AP35_STRPU	Q1ap35	strongyloce
8	1472	35.7	981	2	A2AHE5_MOUSE	A2ahe5	mus musculu
9	1467.5	35.6	981	1	TM16C_HUMAN	Q9byt9	homo sapien
10	1463	35.5	900	2	A1A5Z4_DANRE	A1a5z4	danio rerio
11	1460.5	35.4	921	2	Q1AP37_STRPU	Q1ap37	strongyloce
12	1452.5	35.2	960	1	TM16A_MOUSE	Q8bhy3	mus musculu
13	1450.5	35.2	986	1	TM16A_HUMAN	Q5xxa6	homo sapien
14	1437	34.9	999	1	TM16B_HUMAN	Q9nq90	homo sapien
15	1434.5	34.8	913	2	Q8CFW1_MOUSE	Q8cfw1	mus musculu
16	1419	34.4	896	2	Q6DDQ3_XENLA	Q6ddq3	xenopus lae
17	1413.5	34.3	1014	2	Q175J3_AEDAE	Q175j3	aedes aegyp
18	1413.5	34.3	1117	2	Q0IEX5_AEDAE	Q0iex5	aedes aegyp
19	1412.5	34.3	913	1	TM16E_HUMAN	Q75v66	homo sapien
20	1402.5	34.0	906	2	Q7QDY0_ANOGA	Q7qdy0	anopheles g
21	1382.5	33.5	412	2	Q4SC97_TETNG	Q4sc97	tetraodon n
22	1382.5	33.5	1235	2	Q2M0Y5_DROPS	Q2m0y5	drosophila
23	1378.5	33.4	1219	2	Q9VTS0_DROME	Q9vts0	drosophila
24	1369	33.2	910	1	TM16F_HUMAN	Q4kmq2	homo sapien
25	1367.5	33.2	712	2	Q8NCT7_HUMAN	Q8nct7	homo sapien
26	1366.5	33.1	1613	2	Q4S1F6_TETNG	Q4s1f6	tetraodon n
27	1355.5	32.9	909	2	A6NNM6_HUMAN	A6nnm6	homo sapien
28	1351	32.8	904	1	TM16E_MOUSE	Q75ur0	mus musculu
29	1351	32.8	904	2	Q3V657_MOUSE	Q3v657	mus musculu
30	1346	32.6	871	2	Q8JFT1_DANRE	Q8jft1	danio rerio
31	1344	32.6	926	2	Q8IN71_DROME	Q8in71	drosophila
32	1344	32.6	1075	2	Q9VDV4_DROME	Q9vdv4	drosophila
33	1343	32.6	972	2	Q86P24_DROME	Q86p24	drosophila
34	1336.5	32.4	911	1	TM16F_MOUSE	Q6p9j9	mus musculu
35	1329	32.2	1062	2	Q293M2_DROPS	Q293m2	drosophila
36	1291	31.3	895	2	Q16L02_AEDAE	Q16l02	aedes aegyp
37	1290	31.3	1035	2	Q4SSV5_TETNG	Q4ssv5	tetraodon n
38	1281	31.1	863	2	Q16MH2_AEDAE	Q16mh2	aedes aegyp
39	1251.5	30.4	823	2	Q7QEP9_ANOGA	Q7qep9	anopheles g
40	1227.5	29.8	971	2	Q4REV7_TETNG	Q4rev7	tetraodon n
41	1221	29.6	1017	2	Q29H97_DROPS	Q29h97	drosophila
42	1207	29.3	984	2	Q8MT62_DROME	Q8mt62	drosophila
43	1205	29.2	854	2	Q2VPA8_MOUSE	Q2vpa8	mus musculu
44	1159.5	28.1	1043	2	Q9VYS8_DROME	Q9vys8	drosophila
45	1159.5	28.1	1059	2	Q76NS2_DROME	Q76ns2	drosophila

# ALIGNMENTS

## RESULT 1

TM16G\_HUMAN

ID TM16G\_HUMAN Reviewed; 933 AA.  
AC Q6IWH7; Q6IWH6;  
DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.  
DT 05-JUL-2004, sequence version 1.  
DT 24-JUL-2007, entry version 21.  
DE Transmembrane protein 16G (New gene expressed in prostate) (Prostate

DE cancer-associated protein 5) (IPCA-5) (Dresden-transmembrane protein  
DE of the prostate) (D-TMPP).

GN Name=TMEM16G; Synonyms=NGEP, PCANAP5;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY,  
RP SUBCELLULAR LOCATION, AND TOPOLOGY.

RX PubMed=14981236; DOI=10.1073/pnas.0308746101;

RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,  
RA Hahn Y., Lee B., Pastan I.;

RT "NGEP, a gene encoding a membrane protein detected only in prostate  
RT cancer and normal prostate.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).

RN [2]

RP IDENTIFICATION.

RX PubMed=10613842; DOI=10.1101/gr.9.12.1198;

RA Walker M.G., Volkmuth W., Sprinzak E., Hodgson D., Klingler T.;

RT "Prediction of gene function by genome-scale expression analysis:  
RT prostate cancer-associated genes.";

RL Genome Res. 9:1198-1203(1999).

RN [3]

RP IDENTIFICATION.

RX PubMed=15375614;

RA Katoh M., Katoh M.;

RT "Characterization of human TMEM16G gene in silico.";

RL Int. J. Mol. Med. 14:759-764(2004).

RN [4]

RP ALTERNATIVE SPLICING (ISOFORM 3), TISSUE SPECIFICITY, AND INDUCTION BY  
RP ANDROGEN.

RX PubMed=15761874; DOI=10.1002/pros.20250;

RA Kiessling A., Weigle B., Fuessel S., Ebner R., Meye A., Rieger M.A.,  
RA Schmitz M., Temme A., Bachmann M., Wirth M.P., Rieber E.P.;

RT "D-TMPP: a novel androgen-regulated gene preferentially expressed in  
RT prostate and prostate cancer that is the first characterized member of  
RT an eukaryotic gene family.";

RL Prostate 64:387-400(2005).

RN [5]

RP FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RX PubMed=17308099; DOI=10.1158/0008-5472.CAN-06-2673;

RA Das S., Hahn Y., Nagata S., Willingham M.C., Bera T.K., Lee B.,  
RA Pastan I.;

RT "NGEP, a prostate-specific plasma membrane protein that promotes the  
RT association of LNCaP cells.";

RL Cancer Res. 67:1594-1601(2007).

CC -!- FUNCTION: May play a role in cell-cell interactions.

CC -!- SUBCELLULAR LOCATION: Isoform 1: Cell membrane; Multi-pass  
CC membrane protein. Isoform 2: Cytoplasm, cytosol. Note=Isoform 1  
CC concentrates at sites of cell-cell contact.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1; Synonyms=NGEP-L;

```

CC      IsoId=Q6IWH7-1; Sequence=Displayed;
CC      Name=2; Synonyms=NGEP-S;
CC      IsoId=Q6IWH7-2; Sequence=VSP_026004, VSP_026005, VSP_026006;
CC      Name=3; Synonyms=D-TMPP;
CC      IsoId=Q6IWH7-3; Sequence=VSP_026004, VSP_026007, VSP_026008;
CC      !- TISSUE SPECIFICITY: Specifically expressed in epithelial cells of
CC      the prostate (at protein level).
CC      !- INDUCTION: Up-regulated by androgen.
CC      !- SIMILARITY: Belongs to the TMEM16 family.
CC      !- CAUTION: It is uncertain whether Met-1 or Met-55 is the initiator.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY617079; AAT40139.1; -; mRNA.
DR      EMBL; AY617080; AAT40140.1; -; mRNA.
DR      UniGene; Hs.163909; -.
DR      Ensembl; ENSG00000146205; Homo sapiens.
DR      HGNC; HGNC:31677; TMEM16G.
DR      MIM; 605096; gene.
DR      PharmGKB; PA32980; -.
DR      ArrayExpress; Q6IWH7; -.
DR      GO; GO:0005886; C:plasma membrane; IDA:MGI.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      1: Evidence at protein level;
KW      Alternative splicing; Cytoplasm; Membrane; Polymorphism;
KW      Transmembrane.
FT      CHAIN           1      933      Transmembrane protein 16G.
FT                                     /FTId=PRO_0000289326.
FT      TOPO_DOM        1      355      Extracellular (Potential).
FT      TRANSMEM        356     376      Potential.
FT      TOPO_DOM        377     420      Cytoplasmic (Potential).
FT      TRANSMEM        421     441      Potential.
FT      TOPO_DOM        442     499      Extracellular (Potential).
FT      TRANSMEM        500     520      Potential.
FT      TOPO_DOM        521     550      Cytoplasmic (Potential).
FT      TRANSMEM        551     571      Potential.
FT      TOPO_DOM        572     588      Extracellular (Potential).
FT      TRANSMEM        589     609      Potential.
FT      TOPO_DOM        610     714      Cytoplasmic (Potential).
FT      TRANSMEM        715     735      Potential.
FT      TOPO_DOM        736     763      Extracellular (Potential).
FT      TRANSMEM        764     784      Potential.
FT      TOPO_DOM        785     843      Cytoplasmic (Potential).
FT      TRANSMEM        844     864      Potential.
FT      TOPO_DOM        865     933      Extracellular (Potential).
FT      VAR_SEQ         110     110      Missing (in isoform 2 and isoform 3).
FT                                     /FTId=VSP_026004.
FT      VAR_SEQ         158     180      QDVQDGNNTTVHYALLSASWAVLC -> VRGGCHGQGPRPCI
FT                                     HSVTHDLAA (in isoform 2).
FT                                     /FTId=VSP_026005.
FT      VAR_SEQ         181     933      Missing (in isoform 2).
FT                                     /FTId=VSP_026006.
FT      VAR_SEQ         859     859      H -> VAEAPAGSPIHGMRPRPCALPNSSTW (in

```

FT isoform 3).  
FT /FTId=VSP\_026007.  
FT VAR\_SEQ 860 933 Missing (in isoform 3).  
FT /FTId=VSP\_026008.  
FT VARIANT 67 67 V -> I (in dbSNP:rs2302054).  
FT /FTId=VAR\_032616.  
SQ SEQUENCE 933 AA; 105531 MW; D6FD42578A41D7D3 CRC64;

Query Match 100.0%; Score 4123; DB 1; Length 933;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60  
|  
Db 157 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 216  
  
Qy 61 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 120  
|  
Db 217 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 276  
  
Qy 121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVR 180  
|  
Db 277 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVR 336  
  
Qy 181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240  
|  
Db 337 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 396  
  
Qy 241 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 300  
|  
Db 397 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 456  
  
Qy 301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 360  
|  
Db 457 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 516  
  
Qy 361 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 420  
|  
Db 517 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 576  
  
Qy 421 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 480  
|  
Db 577 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 636  
  
Qy 481 LIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 540  
|  
Db 637 LIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 696  
  
Qy 541 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVA 600  
|  
Db 697 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVA 756  
  
Qy 601 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 660  
|  
Db 757 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 816

Qy 661 SSFAAAHNRTCryRAFRDDDDGHYSQTYWNLLAIRLAFVIVFEHVVFsvGRLLDLLVPDIP 720  
|||||  
Db 817 SSFAAAHNRTCryRAFRDDDDGHYSQTYWNLLAIRLAFVIVFEHVVFsvGRLLDLLVPDIP 876  
  
Qy 721 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ 777  
|||||  
Db 877 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ 933

RESULT 2

TM16G\_MOUSE

ID TM16G\_MOUSE Reviewed; 859 AA.  
AC Q14AT5; Q6IFT5;  
DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.  
DT 29-MAY-2007, sequence version 2.  
DT 24-JUL-2007, entry version 9.  
DE Transmembrane protein 16G (New gene expressed in prostate homolog).  
GN Name=Tmem16g; Synonyms=Ngep;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=C57BL/6J;  
RG The mouse genome sequencing consortium;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).  
RX PubMed=15489334; DOI=10.1101/gr.2596504;  
RG The MGC Project Team;  
RT "The status, quality, and expansion of the NIH full-length cDNA  
RT project: the Mammalian Gene Collection (MGC).";  
RL Genome Res. 14:2121-2127(2004).  
RN [3]  
RP IDENTIFICATION.  
RX PubMed=14981236; DOI=10.1073/pnas.0308746101;  
RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,  
RA Hahn Y., Lee B., Pastan I.;  
RT "NGEP, a gene encoding a membrane protein detected only in prostate  
RT cancer and normal prostate.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).  
CC -!- FUNCTION: May play a role in cell-cell interactions (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein  
CC (By similarity). Note=Concentrates at sites of cell-cell contact  
CC (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q14AT5-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q14AT5-2; Sequence=VSP\_026009, VSP\_026010;  
CC -!- SIMILARITY: Belongsto the TMEM16 family.



http://es/ScoreAccessWeb/GetItem.action?AppId=105525...10-552-515-1\_copy\_157\_933.rup&ItemType=4&startByte=0 (8 of 39)10/10/2008 8:51:52 AM



OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Brown Norway;  
 RX PubMed=15057822; DOI=10.1038/nature02426;  
 RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,  
 RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,  
 RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,  
 RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,  
 RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,  
 RA Fosler C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,  
 RA Pfannkoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,  
 RA Smith D., Lee H.-M., Gustafson E., Cahill P., Kana A.,  
 RA Doucette-Stamm L., Weinstock K., Fechtel K., Weiss R.B., Dunn D.M.,  
 RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,  
 RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,  
 RA Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,  
 RA Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,  
 RA Abramzon S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,  
 RA Ren Y., Song X.-Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,  
 RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,  
 RA Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,  
 RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E.,  
 RA Birney E., Mongin E., Ureta-Vidal A., Woodward C., Zdobnov E.,  
 RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,  
 RA Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,  
 RA Schmidt J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,  
 RA Abril J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,  
 RA Poliakov A., Huebner N., Ganten D., Goesele C., Hummel O.,  
 RA Kreitler T., Lee Y.-A., Monti J., Schulz H., Zimdahl H.,  
 RA Himmelbauer H., Lehrach H., Jacob H.J., Bromberg S.,  
 RA Gullings-Handley J., Jensen-Seaman M.I., Kwitek A.E., Lazar J.,  
 RA Pasko D., Tonellato P.J., Twigger S., Ponting C.P., Duarte J.M.,  
 RA Rice S., Goodstadt L., Beatson S.A., Emes R.D., Winter E.E.,  
 RA Webber C., Brandt P., Nyakatura G., Adetobi M., Chiaromonte F.,  
 RA Elnitski L., Eswara P., Hardison R.C., Hou M., Kolbe D., Makova K.,  
 RA Miller W., Nekrutenko A., Riemer C., Schwartz S., Taylor J., Yang S.,  
 RA Zhang Y., Lindpaintner K., Andrews T.D., Caccamo M., Clamp M.,  
 RA Clarke L., Curwen V., Durbin R.M., Eyraas E., Searle S.M., Cooper G.M.,  
 RA Batzoglu S., Brudno M., Sidow A., Stone E.A., Payseur B.A.,  
 RA Bourque G., Lopez-Otin C., Puente X.S., Chakrabarti K., Chatterji S.,  
 RA Dewey C., Pachter L., Bray N., Yap V.B., Caspi A., Tesler G.,  
 RA Pevzner P.A., Haussler D., Roskin K.M., Baertsch R., Clawson H.,  
 RA Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R.,  
 RA Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M.,  
 RA Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riethman H.,  
 RA Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S.,  
 RA Collins F.S.;  
 RT "Genome sequence of the Brown Norway rat yields insights into  
 RT mammalian evolution."  
 RL Nature 428:493-521(2004).  
 RN [2]  
 RP IDENTIFICATION.  
 RX PubMed=14981236; DOI=10.1073/pnas.0308746101;  
 RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,

```

RA  Hahn Y., Lee B., Pastan I.;
RT  "NGEP, a gene encoding a membrane protein detected only in prostate
RT  cancer and normal prostate.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).
CC  -!- FUNCTION: May play a role in cell-cell interactions (By
CC      similarity).
CC  -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC      (By similarity). Note=Concentrates at sites of cell-cell contact
CC      (By similarity).
CC  -!- SIMILARITY: Belongs to the TMEM16 family.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AABR03068351; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  EMBL; AABR03069029; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  EMBL; AABR03070767; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  EMBL; BK004074; DAA04565.1; -; mRNA.
DR  UniGene; Rn.163084; -.
DR  Ensembl; ENSRNOG00000023427; Rattus norvegicus.
DR  RGD; 1302987; Ngpe.
DR  InterPro; IPR007632; DUF590.
DR  PANTHER; PTHR12308; DUF590; 1.
DR  Pfam; PF04547; DUF590; 1.
PE  2: Evidence at transcript level;
KW  Membrane; Transmembrane.
FT  CHAIN           1      860      Transmembrane protein 16G.
FT                                     /FTId=PRO_0000289328.
FT  TOPO_DOM        1      297      Extracellular (Potential).
FT  TRANSMEM        298     318      Potential.
FT  TOPO_DOM        319     362      Cytoplasmic (Potential).
FT  TRANSMEM        363     383      Potential.
FT  TOPO_DOM        384     441      Extracellular (Potential).
FT  TRANSMEM        442     462      Potential.
FT  TOPO_DOM        463     492      Cytoplasmic (Potential).
FT  TRANSMEM        493     513      Potential.
FT  TOPO_DOM        514     530      Extracellular (Potential).
FT  TRANSMEM        531     551      Potential.
FT  TOPO_DOM        552     652      Cytoplasmic (Potential).
FT  TRANSMEM        653     673      Potential.
FT  TOPO_DOM        674     701      Extracellular (Potential).
FT  TRANSMEM        702     722      Potential.
FT  TOPO_DOM        723     779      Cytoplasmic (Potential).
FT  TRANSMEM        780     800      Potential.
FT  TOPO_DOM        801     860      Extracellular (Potential).
SQ  SEQUENCE      860 AA;  97170 MW;  96BE3CBD6DE96101 CRC64;

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Query Match 84.2%; Score 3472; DB 1; Length 860;  
 Best Local Similarity 85.7%; Pred. No. 1.8e-281;  
 Matches 652; Conservative 36; Mismatches 69; Indels 4; Gaps 2;

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Qy      1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60
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Db     99 QRDVQDEAAAVHYILLSAPWAVLCYYAEDLRLKLPLQELPNQASNWSATLLEWLGIPNIL 158

Qy     61 LEVVPDVPPEYYSCRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 120

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Db	159	LENVPDTPPEYYSCQFKASKLQWFLGSDNQDTFFTSTKRHQILFEILAKTPYGHQKKGLF	218
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Db	219	GIDQLLAEGVFSAAFPLHDGPFVSVPESSQVLGLTQRQVLFKHWARWGKWRKYQPLDHVR	278
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
Db	279	RYFGEKVALYFAWLGFYTGWLLPAAVVGTVVFLAGCFLVFSDVPTQELCHSSDTFDMCPL	338
Qy	241	CLDCPFWLLSSACALAQAGRLFDHGGTVFFSFLMALWAVLLLEYWKRKSATLAYRWDCSD	300
Db	339	CSDCSFWLLSSACTLAQAGRLFDHGGTVFFSFLMALWAVLLLEYWKRKNATLAYRWDCSD	398
Qy	301	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	360
Db	399	YEDIEERPRPQFAATAPMTALNPITGEDEPYFPEKNRVRRLAGSVVLLMMVAVVIMCLV	458
Qy	361	SIILYRAIMAIVVSRGNTLLAAWASRIASLTGSVVNLVFIILISKIYVSLAHVLRWEM	420
Db	459	SIILYRAVMAIIVSKSNNAFLSAWASRIASLTGSVVNLVFIILISKVYVILAQVLRWEM	518
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Db	519	HRTQTAFEDAFTLKVFIFQFVNFYASPVYIAFFKGRFVGYPGNYHTLFGVRNEECPAGGC	578
Qy	481	LIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRRLRSKRRKAGASAGASQGPWEDDY	540
Db	579	LSELAQELLVIMVGKQIINNVEVLVPKLGWCWQK--LCSRKKAG--MGANPAPWEADY	634
Qy	541	ELVPCEGLFDEYLEMVLQFGFVTIFVAAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVA	600
Db	635	ELLPCCEGLFHEYLEMVLQFGFVTIFVAAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVA	694
Qy	601	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP	660
Db	695	ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRVYYSWTRAPDLRGFLNFTLARAP	754
Qy	661	SSFAAAHNRTCryRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDIP	720
Db	755	PTFTSAHNRTCryRAFRDDDGHYSPTYWTLAIRLAFVIVFEHVVFSTGRFLDLLVPDIP	814
Qy	721	ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELS	761
Db	815	ESVEIKVKREYYLAKQALADNEALLGATGVKGEQPPSSEPS	855

RESULT 4

A6QLE6\_BOVIN

ID A6QLE6\_BOVIN Unreviewed; 920 AA.

AC A6QLE6;

DT 21-AUG-2007, integrated into UniProtKB/TrEMBL.

DT 21-AUG-2007, sequence version 1.

DT 21-AUG-2007, entry version 1.

DE Putative uncharacterized protein.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=L1 Hereford; TISSUE=Basal ganglia;  
RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,  
RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,  
RA Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,  
RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,  
RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,  
RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;  
RL Submitted (JUN-2007) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; BC147937; AAI47938.1; -; mRNA.  
PE 2: Evidence at transcript level;  
SQ SEQUENCE 920 AA; 107708 MW; 3AFFC6310F1862CD CRC64;

Query Match 36.5%; Score 1505.5; DB 2; Length 920;  
Best Local Similarity 40.4%; Pred. No. 1.6e-116;  
Matches 328; Conservative 145; Mismatches 270; Indels 69; Gaps 20;

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Db 122 NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFMSRIDKQISRFRRLPKK 181  
  
Qy 58 NVLL--EVVPDVPP-EYYSCRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGH 114  
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Db 182 PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKDTFFNATRSRIVHHILQRIKY-E 239  
  
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Qy 175 PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS 234  
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Db 300 PLDLVRRYFGEKIGLYFAWLGWYTGMFLPAAFIGLFVFLYGVITLDHCQVSKEVCQATDI 359  
  
Qy 235 FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLA 293  
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Qy 294 YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV 352  
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Qy 353 AVVVMCLVSIILYRAIMAIIVSRSGNTLLA-AWA-----SRIASLTGSVV--NLVFILIL 404  
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Db 479 CVVIAAVFGIVIYRVVTV-----STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLL 530

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ID      TM16D_HUMAN                               Reviewed;           955 AA.
AC      Q32M45; Q8NAJ0; Q8NB39; Q8NB53;
DT      29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
DT      06-DEC-2005, sequence version 1.
DT      21-AUG-2007, entry version 17.
DE      Transmembrane protein 16D.
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OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).
RC      TISSUE=Brain, and Prostate;
RX      PubMed=14702039; DOI=10.1038/ng1285;
RA      Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA      Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA      Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA      Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA      Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA      Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA      Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA      Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

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RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,  
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,  
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,  
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RX PubMed=15489334; DOI=10.1101/gr.2596504;  
 RG The MGC Project Team;  
 RT "The status, quality, and expansion of the NIH full-length cDNA  
 RT project: the Mammalian Gene Collection (MGC).";  
 RL Genome Res. 14:2121-2127(2004).  
 RN [3]  
 RP IDENTIFICATION.  
 RX PubMed=12739008;  
 RA Katoh M., Katoh M.;  
 RT "FLJ10261 gene, located within the CCND1-EMS1 locus on human  
 RT chromosome 11q13, encodes the eight-transmembrane protein homologous  
 RT to C12orf3, C11orf25 and FLJ34272 gene products.";  
 RL Int. J. Oncol. 22:1375-1381(2003).  
 CC -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein  
 CC (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
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 CC Name=2;  
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 CC Name=3;  
 CC IsoId=Q32M45-3; Sequence=VSP\_025741, VSP\_025743;  
 CC Note=No experimental confirmation available;  
 CC -!- SIMILARITY: Belongs to the TMEM16 family.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AK091540; BAC03688.1; ALT\_INIT; mRNA.  
 DR EMBL; AK091591; BAC03704.1; -; mRNA.

DR EMBL; AK092596; BAC03924.1; -; mRNA.  
DR EMBL; BC109308; AAI09309.1; -; mRNA.  
DR UniGene; Hs.58785; -.  
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DR HGNC; HGNC:23837; TMEM16D.  
DR MIM; 610111; gene.  
DR PharmGKB; PA134975112; -.  
DR ArrayExpress; Q32M45; -.  
DR InterPro; IPR007632; DUF590.  
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DR Pfam; PF04547; DUF590; 1.  
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FT TRANSMEM 425 445 Potential.  
FT TRANSMEM 506 526 Potential.  
FT TRANSMEM 548 568 Potential.  
FT TRANSMEM 596 616 Potential.  
FT TRANSMEM 716 736 Potential.  
FT TRANSMEM 769 789 Potential.  
FT TRANSMEM 886 906 Potential.  
FT COILED 918 953 Potential.  
FT CARBOHYD 824 824 N-linked (GlcNAc. . .) (Potential).  
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FT /FTId=VSP\_025741.  
FT VAR\_SEQ 19 54 EGGVDLQGYQLDMQILPDGPKSDVDFSEILNAIQEM -> V  
FT (in isoform 2).  
FT /FTId=VSP\_025742.  
FT VAR\_SEQ 466 512 Missing (in isoform 3).  
FT /FTId=VSP\_025743.  
FT VARIANT 115 115 G -> A (in dbSNP:rs34162417).  
FT /FTId=VAR\_032453.  
FT CONFLICT 209 209 F -> L (in Ref. 1; BAC03704).  
SQ SEQUENCE 955 AA; 111462 MW; 9A9348C61A4F20AF CRC64;

Query Match 36.3%; Score 1498.5; DB 1; Length 955;  
Best Local Similarity 40.3%; Pred. No. 6.4e-116;  
Matches 327; Conservative 145; Mismatches 271; Indels 69; Gaps 20;

Qy 8 NTTVHYALLSASWAVLCYYAEDRLRLKLPLQE----LPNQASNWS-----AGLLAWLGIP 57  
|: : : | | | || || : ::| : || : | : ||  
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Qy 58 NVLL--EVVPDVPP-EYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGH 114  
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Db 217 PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA TRSRIVHHILQRIKY-E 274  
  
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Db 275 EGKNKIGLNRLLTNGSYEAAFPLHEGSYRSKNSIRTHGAENHRHLLYECWASWGVWYKYQ 334  
  
Qy 175 PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS 234

Db	335	PLDLVRRYFGEKIGLYFAWLGWYTGMFLPAAFIGLFLVFLYGVTTLDHSQVSKEVCQATDI	394
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Db	395	I-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFFAVFMVWATVFLEFWKRRRAVIA	453
Qy	294	YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV	352
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Qy	353	AVVVMCLVSIILYRAIMAIIVSRSGNTLLA-AWA-----SRIASLTGSVV--NLVFILIL	404
Db	514	CVVIAAVFGIVIRVVTV-----STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLL	565
Qy	405	SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNY	464
Db	566	NVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAFFLGRFTGHPGAY	625
Qy	465	HTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRLRSKKR	523
Db	626	LRLINRWRLEECHPSGCLIDLQMGIIMVLKQTNWNNFMELGYPLIQNWWTR---RKVRQ	682
Qy	524	KAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLALLNNW	581
Db	683	EHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNI	742
Qy	582	VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR	641
Db	743	IEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVIAITSDFIPRLVYA	802
Qy	642	W-----TRAHDLRGFLNFTLA-----RAPSSFAAAHNRTCRYRAFR	677
Db	803	YKYGPCAGQGEGAGQKCMVGYNASLSVFRISDFENRSEPESDGSEFSGTPLKYCRYRDYR	862
Qy	678	DDDGH-----YSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYY	732
Db	863	DPPHSLVPYGYTLQFVHVLAAARLAFIIVFEHLVFCIKHLISYLIPDLPKDLRDRMRREKY	922
Qy	733	LAKQALAENEVLFGTNGTKDEQPKGSELSSHW	764
Db	923	LIQEMMYEAELERLQKERKERKKNGKAHHNEW	954

RESULT 6

Q1AP36\_STRPU

ID	Q1AP36_STRPU	Unreviewed;	903 AA.
AC	Q1AP36;		
DT	11-JUL-2006,	integrated into UniProtKB/TrEMBL.	
DT	11-JUL-2006,	sequence version 1.	
DT	24-JUL-2007,	entry version 6.	
DE	122 kDa protein TMEM16	(Fragment).	
OS	Strongylocentrotus purpuratus	(Purple sea urchin).	
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;		
OC	Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;		
OC	Strongylocentrotus.		



OX NCBI\_TaxID=7668;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Coelomocyte;  
 RA Galindo B.E., Moy G.W., Vacquier V.D.;  
 RT "A 122 kDa protein from Strongylocentrotus purpuratus embryo belongs  
 RT to TMEM16 protein family."  
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.  
 CC -----  
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 CC -----  
 DR EMBL; DQ020165; AAY82886.1; -; mRNA.  
 DR UniGene; Spu.15325; -.  
 DR InterPro; IPR007632; DUF590.  
 DR PANTHER; PTHR12308; DUF590; 1.  
 DR Pfam; PF04547; DUF590; 1.  
 PE 2: Evidence at transcript level;  
 FT NON\_TER 1 1  
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 Qy 62 EVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLG 121  
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 Db 172 EEYVKPEPDVFTAPFIRDRASEFI-MESQDTFFPNNIRNRVVYEILERMRYDANDPAKFG 230  
  
 Qy 122 IHQLLAEGVLSAAFPLHDGPFKTP---PEGPQAPRLNQRQVLFQHWARWGKWNKYQPLD 177  
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 Qy 178 HVERRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEM 237  
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 Db 287 LIRRYFGEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLPSSVVVQEICDGTDIIM 345  
  
 Qy 238 CPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRW 296  
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 Db 346 CPLCDKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCEFWKRRQNTIDYDW 405  
  
 Qy 297 DCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVV 356  
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 Qy 357 MCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNLVFILILSKIYVSLAHVLT 416  
 : :: |:| : : : : || | |:| | : :: |:| :| :| ||  
 Db 466 AAVMTVIVYRIVVKTAFIDQEFISSYASIITSVTASMISLILIMILQILYERIAVWLT 525  
  
 Qy 417 RWEHRTQTKFEDAFTLKVFIQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGV-RNEEC 475  
 |:| |:| :| :| | : ::| |||:| : || || || | | :| :| :| | ||

Db 526 NLELHRTETEDSFTFKMYLFAFVNYYSTSFYIAFFKGRLPGTPADYGRVFGIWRQEEC 585

Qy 476 AAGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWQKQFRLRSKKRKAGASAGASQGP 535  
||: || : : | || | | : : | | : | : |

Db 586 DPAGCMQELFINIAITMCGKQFFNNFMELAMPVLMNFWRS-RTGRKEEKSGK---GRYEQ 641

Qy 536 WEDDYELVPC--EGLFDEYLEMVLQFGFVTIFVAACPLAPLFPALLNNWVEIRLDARKFVC 593  
| | | : | | | | | | : | | | | | | | | | | | | : | | | |

Db 642 WEQDADLADLGRGLFKEYLEMVVQFGFSTIFVAAPLAPLFPALLNNLVEVRLDAYKFIS 701

Qy 594 EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPR---AYYRWTRAHDLRG 650  
: | | | | : | | | | | : | | : : | : : | : | : | | | | |

Db 702 QLRRPVAKRAQDIGAWYAILVTVGNSVLTNALVIAFTSEFIPRQVFKYYYGGPEATLNG 761

Qy 651 FLNFTLA-----RAPSSFAAAHNRT-----CRYRAFRDDDGHYSQT 686  
: | : : | : | | | | | | | | | | | | | : | | : |

Db 762 YTNWSLSYFNTVDMQNDSKPTDPSYPRVGDEDTTDPNYGLNVSVCRYRGNYDE--HYNVT 819

Qy 687 --YWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDIPESVEIKVKREYYLAKQAL 738  
| | : : | : | | : : | | | : : | | | | | : | |

Db 820 LDYWLVIAlKLAfillYEHFVLFtkFFVAYIIPDMPEFVKNQIKRETYLGQQAL 873

RESULT 7

Q1AP35\_STRPU

ID Q1AP35\_STRPU Unreviewed; 921 AA.

AC Q1AP35;

DT 11-JUL-2006, integrated into UniProtKB/TrEMBL.

DT 11-JUL-2006, sequence version 1.

DT 24-JUL-2007, entry version 6.

DE 122 kDa protein TMEM16.

OS Strongylocentrotus purpuratus (Purple sea urchin).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;

OC Strongylocentrotus.

OX NCBI\_TaxID=7668;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Testis;

RA Galindo B.E., Vacquier V.D.;

RT "Phylogeny of the TMEM16 Protein Family: Some Are Over Expressed in

RT Cancer.";

RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.

CC -----

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CC -----

DR EMBL; DQ020166; AAY82887.1; -; mRNA.

DR UniGene; Spu.15325; -.

DR InterPro; IPR007632; DUF590.

DR PANTHER; PTHR12308; DUF590; 1.

DR Pfam; PF04547; DUF590; 1.

PE 2: Evidence at transcript level;

SQ SEQUENCE 921 AA; 106711 MW; C3F912A32528F059 CRC64;

Query Match 35.8%; Score 1475.5; DB 2; Length 921;

Best Local Similarity 40.4%; Pred. No. 5.2e-114;  
Matches 311; Conservative 142; Mismatches 266; Indels 51; Gaps 15;

Qy	6	DGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVP	65
		: :     : :     : :     : :   :   :	
Db	136	DGRT--FFVKVHAPWDLMTRYAEELKIKMPIEENNMEEPVNVFNCIDKLWTPFELSEYV	193
Qy	66	DVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQ	125
		: : :   : :   : :         :   : : :     :	
Db	194	KPEPDVFTAPFIRDRASEFI-MESQDTFFPNIRNRVVEILERMRYDANDPAKFGIDHL	252
Qy	126	LAEGVLSAAFPLHDGPFKTP----PEGPQAPRLNQRVLFQHWARWGKWNKYQPLDHVRR	181
		:       :       :   :       :     :       :	
Db	253	IANGSYFAAYPLHEGDYKSKHSLTHGPQ---NDRHLLYEEWARPGRWYKKQPLDLIRR	308
Qy	182	YFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC	241
		: :                 :     :   :	
Db	309	YFGEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLPSSVVVQEICAGTDII-MCPLC	367
Qy	242	-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD	300
		:     :   : :       :     :     :   :	
Db	368	DKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCEFWKRRQNTIDYDWDLFG	427
Qy	301	YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV	360
		:   :     :       :         :         :   : : :	
Db	428	FEEQEENIRPEFEAKAPDRRVSPITNLTEPYMKFSRKFPFSASIASIFFMILLVMAAVM	487
Qy	361	SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSSVNLVFIILISKIYVSLAHVLTRWEM	420
		: :   :   : : : : :   :   : : :   :   :   :	
Db	488	TVIVYRIVVKTAIFAIDQEFISSYASIITSVTASMISLILIMILQILYERIAVRLTNLEL	547
Qy	421	HRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTLFGV-RNEECAAGG	479
		:   : :       : :       :	
Db	548	HRTETEYEDSFTFKMYLFAFVNYYSTSFYIAFFKGRLPGTPADYGRVFGIWRQEECDPAG	607
Qy	480	CLIELAQELLVIMVGKQVINNMQEVLIPLKKGWWQKFRRLRSKRRKAGASAGASQGPWEDD	539
		:     : :           : :   :   :   :	
Db	608	CMQELFINIAITMCGKQFFNNFMELAMPVLMNFWRS-RTGRKEEKSGK---GRYEQWEQD	663
Qy	540	YELVPC--EGLFDEYLEMVLQFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRR	597
		:             :	
Db	664	ADLADLGPRGLFKEYLEMVVQFGFSTIFVAAPLAPLFAALLNNLVEVRLDAYKFISQLRR	723
Qy	598	PVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR---AYRWTRAHDLRGFLNF	654
		:             :     : :   : :     : :	
Db	724	PVAKRAQDIGAWYAILVTGNLSVLTNALVIAFTSEFIPRQVFKEYYYGGPEATLNGYTNW	783
Qy	655	TLA-----RAPSSFAAAHNRT-----CRYRAFRDDDGHYSQT--YW	688
		:   :                           :     :	
Db	784	SLSYFNTVDMQNDSKPTDPSYPRVGDEDTTDPNYGLNVSVCRYRGNYDE--HYNVTLDYW	841
Qy	689	NLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQAL	738
		: :     :     : :     : :     : :     :	
Db	842	LVIAIKLAFILLYEHFVLFVKFFVAYIIPDMPEFVKNQIKRETYLGQQAL	891



Db	262	PMVLDKSAFPELEESDCYTGPFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYEN	320
Qy	113	GHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT----PPEGPQAPRLNQEQVLFQHWARWG	168
		:   : :        :  : :        : ::	
Db	321	GISK---VGIRKLITNGSYIAAFPHEGAYKSSLPKTHGPQ---NNRHLLYERWARWG	373
Qy	169	KWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQEL	228
		:     :      :      :      :           : :  :	
Db	374	MWYKHQPLDLIRMYFGEKIGLYFAWLGWYTGM LIPAAVVGLCVFFYGLVTMNESQVSQEI	433
Qy	229	CGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKR	287
		: :        :    : :    :    :     : : : :    :    :	
Db	434	CKATEVF-MCPLCDKNCSLQRLNDSCIYAKVTYLFDNGGTVFFAIFMAIWATVFLEFWKR	492
Qy	288	KSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSV	346
		: :        :::                :   :   :  :	
Db	493	RRSILTYTWDLIEWEEEEETLRPQFEAKYYRMEVINPITGKPEPHQPSSDKVTRLLVSVS	552
Qy	347	VIVVMVAVVVMCLVSIILYR-AIMAIVVSRSNTLLAAWASRIASLTGSV-VNLVFILIL	404
		:: : : ::::    :     :   :   :   :   : :	
Db	553	GIFFMISLVITAVFAVVYRLVMEQFASFKNFVKQHW--QFATSGAAVCINFIIIMLL	610
Qy	405	SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNY	464
		:   : ::       ::: :    : :                 :	
Db	611	NLAYEKIAYLLTNLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKY	670
Qy	465	HTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV LIPKLKGWWQKFR LRSKKR	523
		:              :  : :       :      :   : :    : :	
Db	671	NKLFERWRLEECHPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----	725
Qy	524	KAGASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNNW	581
		: :	
Db	726	KRGIQ-DASIPQWENDWNLQPMNIHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNI	784
Qy	582	VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR	641
		:          :   :              :    : : :  : :	
Db	785	IEIRLDAYKFVTQWRRPLPARATDIGIWL GILEGIGILAVITNAFVIAITSDYIPRFVYE	844
Qy	642	W-----TRAHDLRGFLNFTLARAP-SSFAAAHNRTC RYRAFR-----DDDGHYSQ	685
		: :  : :  : :   :     :  : :	
Db	845	YKYGPCANHVKQENENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDRGPPWSSKPYEFTL	904
Qy	686	TYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVL F	745
		:       :    :    :   :   : : :::    : :    :	
Db	905	QYWHILAAARLAFIIVFEHLVFGIKSFIAYLIPDIPKGLRERIRREKYL VQEMMYEAE L--	962
Qy	746	GTNGTKDEQPKGSELSSHW	764
		: : :   :	
Db	963	-EHLQQQRRKSGQPIHHEW	980

RESULT 9

TM16C\_HUMAN

ID TM16C\_HUMAN

Reviewed;

981 AA.

AC Q9BYT9;

DT 16-JAN-2004, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2001, sequence version 1.  
DT 24-JUL-2007, entry version 31.  
DE Transmembrane protein 16C.  
GN Name=TMEM16C; Synonyms=C11orf25; ORFNames=GENX-3947;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RA Rosier M.F., Toselli E., Segurens-Soury B., Auffray C., Devignes M.D.;  
RT "Predominant brain expression and full-length characterization of a  
RT novel human 6.6-Kb transcript mapping at 11p14 in the telomeric part  
RT of WAGR locus.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
CC -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein  
CC (Probable).  
CC -!- SIMILARITY: Belongs to the TMEM16 family.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AJ300461; CAC32454.1; -; mRNA.  
DR UniGene; Hs.91791; -.  
DR Ensembl; ENSG00000134343; Homo sapiens.  
DR KEGG; hsa:63982; -.  
DR HGNC; HGNC:14004; TMEM16C.  
DR MIM; 610110; gene.  
DR PharmGKB; PA25489; -.  
DR ArrayExpress; Q9BYT9; -.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
KW Membrane; Transmembrane.  
FT CHAIN 1 981 Transmembrane protein 16C.  
FT /FTId=PRO\_0000072565.  
FT TRANSMEM 398 420 Potential.  
FT TRANSMEM 471 490 Potential.  
FT TRANSMEM 553 575 Potential.  
FT TRANSMEM 590 612 Potential.  
FT TRANSMEM 642 664 Potential.  
FT TRANSMEM 759 781 Potential.  
FT TRANSMEM 809 831 Potential.  
FT TRANSMEM 904 926 Potential.  
SQ SEQUENCE 981 AA; 114655 MW; 15A3276420912393 CRC64;

Query Match 35.6%; Score 1467.5; DB 1; Length 981;  
Best Local Similarity 40.9%; Pred. No. 2.6e-113;  
Matches 313; Conservative 149; Mismatches 245; Indels 59; Gaps 21;

Qy 20 WAVLCYYAEDLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNVLLE--VVPDV 67  
| || ||| | :::| : : : : |: ::| ||:  
Db 214 WDTLCKYAERLNIRMPFRKKCYTDGRSKSMGRMQTYFRRIKDWMAQNPMVLDKSAFPDL 273

Qy	68	-PPEYYSCRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQ	124
		:   :   : :   : :   :   :   :   :   :   :   :	
Db	274	EESDCYTGPFSRARIHFI-INNKDTFFSNATRSRIVYHMLERTKYENGISK---VGIRK	329
Qy	125	LLAEGVLSAAFPLHDGPFKT----PPEGPQAPRLNQSQVLFQHWARWGKWNKYQPLDHVR	180
		:           :   :   :         :   :   :         :	
Db	330	LINNGSYIAAFPPHEGAYKSSQPIKTHGPQ----NNRHLLYERWARWGMWYKHQPLDLIR	385
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
		:           :       :         : :   :   :   :	
Db	386	LYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNNSQVSQEICKATEVF-MCPL	444
Qy	241	C-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCS	299
		:     : :     :     :         :   :   :   :   :   :	
Db	445	CDKNCSLQRLNDSCIYAKVTYLFDNNGGTVFFAIFMAIWATVFLEFWKRRRSILTWTDLI	504
Qy	300	DYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMC	358
		: :   :                 :   :   :   :   :   :   :   :	
Db	505	EWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSSDKVTRLLVSVSGIFFMISLVITA	564
Qy	359	LVSIIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSKIYVSLAHVLT	416
		: : : :   :     :   :   :   :   :   :   :   :   :   :	
Db	565	VFGVVVYRLVMEQFASFKNFQYKQYW--QFATSAAAVCINFIIIMLLNLAYEKIAYLLT	622
Qy	417	RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEEC	475
		: : : :   :     :   :                 :   :	
Db	623	NLEYPRTSESEWENSFALKMFQFVNLNSSIFYIAFFLGRFVGHPGKYNKLFDRWRLEEC	682
Qy	476	AAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWQKFRRLRSKKRKAGASAGASQGP	535
		:   : :       :     :   :   :   : :	
Db	683	HPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----KRGIH-DASIPQ	736
Qy	536	WEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKFVC	593
		:   :                                     :	
Db	737	WENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNIIEIRLDAYKFVT	796
Qy	594	EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRW-----T	643
		: :     :               :     :     :   :   :   :   :	
Db	797	QWRRPLPARATDIGIWLGILEGIGILAVITNAFVIAITSDYIPRFVYKYGPCANHVEP	856
Qy	644	RAHDLRGFLNFTLARAP-SSFAAAHNRTCryAFR----DDDGHYSTYWNLLAIRLAF	697
		:   : : :   : :   :     :   : : :   : :   : :   :	
Db	857	SENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQYWHILAAARLAF	916
Qy	698	VIVFEHVVFVSGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEV	743
		:       :   : :   :   : : : : : :   : : :   :	
Db	917	IIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLQEMMYEAEI	962

RESULT 10

A1A5Z4\_DANRE

ID A1A5Z4\_DANRE Unreviewed; 900 AA.

AC A1A5Z4;

DT 23-JAN-2007, integrated into UniProtKB/TrEMBL.

DT 23-JAN-2007, sequence version 1.  
 DT 24-JUL-2007, entry version 6.  
 DE Zgc:158430.  
 GN ORFNames=zgc:158430;  
 OS Danio rerio (Zebrafish) (Brachydanio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RG NIH MGC Project;  
 RL Submitted (DEC-2006) to the EMBL/GenBank/DDBJ databases.  
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 CC -----  
 DR EMBL; BC128870; AAI28871.1; -; mRNA.  
 DR UniGene; Dr.108272; -.  
 DR ZFIN; ZDB-GENE-061215-108; zgc:158430.  
 DR InterPro; IPR007632; DUF590.  
 DR PANTHER; PTHR12308; DUF590; 1.  
 DR Pfam; PF04547; DUF590; 1.  
 PE 2: Evidence at transcript level;  
 SQ SEQUENCE 900 AA; 105263 MW; DB86567CCE3D153E CRC64;

Query Match 35.5%; Score 1463; DB 2; Length 900;  
 Best Local Similarity 39.0%; Pred. No. 5.6e-113;  
 Matches 308; Conservative 159; Mismatches 244; Indels 78; Gaps 18;



Db	98	HYLKIHAPWEVLATYADVLKIKVPFKVSDIPKAREVP-----LEWLSHPFRLPEN	147
Qy	64	VPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHE---KKNLL	120
Db	148	IMRPEPDYFTAPFDKSKVDFFL-IDDKDTFFFPSTRNRIVYYILTRCPYYKEDRKEKDKT	206
Qy	121	GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQQRQVLFQHWARWGKWNKYQPLDHVR	180
Db	207	GINRLLNNGTYTSAAYPLHDCRYWKKAQDMQCE--SERYHLYRYWARFLCFYKEQPLNLIK	264
Qy	181	RYFGEKVALYFAWLGFYTGWLLPAAVVGTLLVFLVGCFLVFSDIPTQELCGSK--DSFEMC	238
Db	265	KYYGEKIGIYFAWLGFYTEMLFYAAVMGVICFVYGVLSYEDNITSKEICDPKIGGMIVMC	324
Qy	239	PLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWD	297
Db	325	PLCDKKCSYWKLNSTCLSSWQSHLFDNEGTVFFAMFMGIWVTLFLEFWKRRQARLEYEWD	384
Qy	298	CSDYEDTEE--RPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVV	355
Db	385	LVDFFFFEQQLQIRPEYEQKCTGRRNLNRTQEMEPYLPFPSPKCARFCLSGATVLFWTCLI	444
Qy	356	VMCLVSIILYR----AIMAIVVSRSGNTLLAAWASRI-----ASLTGSVVNLVFILILSK	406
Db	445	VACIMGVIAYRLAVYAAFASVMKDSSTSКИQLVGSLITPQLATSVTASCINFVIILILNF	504
Qy	407	IYVSLAHVLTWRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHT	466
Db	505	LYEHVAIWITDMEIPKTHLEYENKLTMKMFMFQFVNYYSSCFYVAFFKGKFGVYPGNYSY	564
Qy	467	LFG---VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRRLRSKK	522
Db	565	MFGKWSTLRNEECAPGGCLIELTQLLIVMAGKQMVGNVQEALLPLVRNWW-----SS	617
Qy	523	RKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNN	580
Db	618	RKGRSHPESTYSRWEQDHDLDQNF SQFGLFYEYLEMVIQFGFITLFVASFPLAPLLALFNN	677
Qy	581	WVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPR---	637
Db	678	ILEVRVDAWKFTTQFRRPMAAKARNIGAWEEILNVVAIMSVVTNAFIMAFTSDMIPRLVY	737
Qy	638	--AYYRWTRAHDLRGFLNFTLA-----RAPSSFAAAHNRTCRYRAFRDD	679
Db	738	LYAYHPGIEA-NMTGYITNSLSIYNISQIPEDNLPEAGENPSWFNSSTITTCRYRDYRYP	796
Qy	680	DGH---YSQT--YWNLLAIRLAFVIVFEHVVFVSGRLLDLLVPDIPESVEIKVKREYYLA	734
Db	797	PGHLRQYTHTMQFWHILAAKLAFIIIMEHVVFVVKFFVAWLIPDVPSEVKARIKRERFLV	856
Qy	735	KQALAENEV	743
Db	857	QEYLNHYEV	865

RESULT 11

Q1AP37\_STRPU

ID Q1AP37\_STRPU Unreviewed; 921 AA.  
AC Q1AP37;  
DT 11-JUL-2006, integrated into UniProtKB/TrEMBL.  
DT 11-JUL-2006, sequence version 1.  
DT 24-JUL-2007, entry version 6.  
DE 122 kDa protein TMEM16.  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Galindo B.E., Moy G.W., Vacquier V.D.;  
RT "A 122 kDa protein from Strongylocentrotus purpuratus embryo belongs  
RT to TMEM16 protein family."  
RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; DQ020164; AAY82885.1; -; mRNA.  
DR UniGene; Spu.15325; -.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
SQ SEQUENCE 921 AA; 106699 MW; 9A516A5DCA1ADCCC CRC64;

Query Match 35.4%; Score 1460.5; DB 2; Length 921;  
Best Local Similarity 40.1%; Pred. No. 9.4e-113;  
Matches 309; Conservative 140; Mismatches 270; Indels 51; Gaps 15;

Qy 6 DGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVP 65  
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Db 136 DGRT--FFVKVHAPWDLMTTRYAEELKIKMPIEENNMEEPVNVFNCLDKLWTPFELSEYV 193  
  
Qy 66 DVPPEYYSCRFRVNKLPRFLGSDNQDTFFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQ 125  
|: :: | :: |: ::||| | : |:::| | : | | |  
Db 194 KPEPDVFTAPFIRDRASEFI-MESQDTFFPNNIRNRVVYEILERMRYDANDPTKFGIDHL 252  
  
Qy 126 LAEGLVLSAAFPLHDGPFKTP----PEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRR 181  
:| | ||:|::| :|: ||| | | :|: ||| |::| :|  
Db 253 IANGSYFAAYPLHEGDYKSKHSLTHGPQ----NDRHLLYEEWARSGRWYKKQPLDLIRC 308  
  
Qy 182 YFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC 241  
||||: :|| ||||| | | || :|| | : | : ||:| | ||||  
Db 309 YFGEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLPSSVVVQEICAGTDII-MCPLC 367  
  
Qy 242 -LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 300  
||:| || :| : : |||: ||||: ||:| | : |::| :|: | |  
Db 368 DKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCEFWKRRQNTIDYDWDLFG 427

http://es/ScoreAccessWeb/GetItem.action?AppId=10552...0-552-515-1\_copy\_157\_933.rup&ItemType=4&startByte=0 (27 of 39)10/10/2008 8:51:52 AM

RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).  
 RC STRAIN=C57BL/6, and Czech II; TISSUE=Eye, and Mammary tumor;  
 RX PubMed=15489334; DOI=10.1101/gr.2596504;  
 RG The MGC Project Team;  
 RT "The status, quality, and expansion of the NIH full-length cDNA  
 RT project: the Mammalian Gene Collection (MGC).";  
 RL Genome Res. 14:2121-2127(2004).  
 CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein  
 CC (By similarity). Cytoplasm (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q8BHY3-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q8BHY3-2; Sequence=VSP\_025672;  
 CC -!- SIMILARITY: Belongs to the TMEM16 family.  
 CC -!- SEQUENCE CAUTION:  
 CC Sequence=BAC35051.1; Type=Miscellaneous discrepancy; Note=Wrong choice of frame;  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AK028991; BAC26230.1; ALT\_INIT; mRNA.  
DR EMBL; AK029329; BAC26398.1; ALT\_INIT; mRNA.  
DR EMBL; AK052589; BAC35051.1; ALT\_SEQ; mRNA.  
DR EMBL; BC006062; AAH06062.1; ALT\_INIT; mRNA.  
DR EMBL; BC062959; AAH62959.1; -; mRNA.  
DR UniGene; Mm.26700; -.  
DR Ensembl; ENSMUSG00000031075; Mus musculus.  
DR MGI; MGI:2142149; Tmem16a.  
DR ArrayExpress; Q8BHY3; -.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
KW Alternative splicing; Cytoplasm; Glycoprotein; Membrane;  
KW Transmembrane.  
FT CHAIN 1 960 Transmembrane protein 16A.  
FT /FTId=PRO\_0000288436.  
FT TOPO\_DOM 1 333 Cytoplasmic (Potential).  
FT TRANSMEM 334 354 Potential.  
FT TOPO\_DOM 355 402 Extracellular (Potential).  
FT TRANSMEM 403 423 Potential.  
FT TOPO\_DOM 424 493 Cytoplasmic (Potential).  
FT TRANSMEM 494 514 Potential.  
FT TOPO\_DOM 515 539 Extracellular (Potential).  
FT TRANSMEM 540 560 Potential.  
FT TOPO\_DOM 561 581 Cytoplasmic (Potential).  
FT TRANSMEM 582 602 Potential.  
FT TOPO\_DOM 603 705 Extracellular (Potential).  
FT TRANSMEM 706 726 Potential.  
FT TOPO\_DOM 727 765 Cytoplasmic (Potential).  
FT TRANSMEM 766 786 Potential.  
FT TOPO\_DOM 787 856 Extracellular (Potential).  
FT TRANSMEM 857 877 Potential.  
FT TOPO\_DOM 878 960 Cytoplasmic (Potential).  
FT CARBOHYD 806 806 N-linked (GlcNAc. . .) (Potential).  
FT VAR\_SEQ 448 451 Missing (in isoform 2).  
FT /FTId=VSP\_025672.  
SQ SEQUENCE 960 AA; 110916 MW; BFD0112FD310CE88 CRC64;

Query Match 35.2%; Score 1452.5; DB 1; Length 960;  
Best Local Similarity 40.0%; Pred. No. 4.6e-112;  
Matches 330; Conservative 156; Mismatches 257; Indels 81; Gaps 22;

Qy 6 DGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLL 62  
| : | : | : : | | | | | | : : : : : : : | | : | : | :  
Db 145 DEDTKIHGVGFVKIHAPWHVLCREAEFLKLKMPTKKVYHISE--TRGLLK--TINSVLQK 200  
  
Qy 63 VVPDVPPEYYSCRFRVNKLPRFLGS-----DNQDTFFTSTKRHQILFEILAKTPYG 113  
: : | : | : | : : : : | | | : : | : | : | : | : |  
Db 201 ITDPIQPKVAEHRPQTTKRLSYFSSREKQHLFDLTD RDSFFDSKTRSTIVYEILKRTTCT 260  
  
Qy 114 HEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKY 173  
| : : | | | | | | : : | | : : : : | : | : | : |

Db	261	KAKYS-MGITSLLANGVYSAAYPLHDGDY-----EGDNV-EFNDRKLLYE EWASYGVFYKY	314
Qy	174	QPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKD	233
		:     :                         :     :     :             :     :	
Db	315	QPIDLVRKYFGEKVGLYFAWLGAYTQMLIPASIVGVIVFLYGCATVDENIPSMEMCDQRY	374
Qy	234	SFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATL	292
		:             :   :           :       :               :	
Db	375	NITMCPLCDKTCSYWKMSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQMRL	434
Qy	293	AYRWDCSDYEDTEE----RPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLA	343
		: :   :         :       :       :	
Db	435	NYRWDLTGFE EEEEEAVKDHPRAEYEARVLEKSLRKESRNKET--DKVKLTWRDRFPAYFT	492
Qy	344	GSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNVLVFILI	403
		:     :     : :   :       : : : : : : :   : :         : :	
Db	493	NLVSIIFMIAVTFAIVLGVIIYRISTAAALAMNSSPSVRSNIRVTVTATAVIINLVIIIL	552
Qy	404	LSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGN	463
		: :   :       :   : :     :       : :       :   :                 :	
Db	553	LDEVYGC IARWLT KIEVPKTEKSFEERLT FKAFL LKFVNSYTPIFYVAFFKGRFVGRPGD	612
Qy	464	YHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLRSK	521
		:                 :     :     :       :   :     :   : : :     :	
Db	613	YVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKFIRYKLRRQ	672
Qy	522	KRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNNW	581
		: :     :               :     :         :	
Db	673	SPSDREEYVKKRQRYEVDNFNLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPL FALLNNI	732
Qy	582	VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR	641
		:         :                 :         :             :     :     :	
Db	733	IEIRLDAKKFVTELRRPVAIRAKDIGIWNILRGVGKLAVIINAFVISFTSDFIPRLVYL	792
Qy	642	WTRAHD--LRGFLNFTLARAPSSF-----AAAHN-----RTCryRAFRD---DD	680
		: : : :     :                         :     :     :     : :	
Db	793	YMYSQNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPWSE	848
Qy	681	GHY--SQTYWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDIPESVEIKVKREYYL-----	733
		: :   :                 : : :   : :       : : : :	
Db	849	HKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQ QIHKEKVL MVELF	908
Qy	734	-----AKQALAENEVLFGTNGTKDEQPKGSELSSHWTPTVPKA	772
		: : : :   :   : : :   :	
Db	909	MREEQGKQQLLDTWM-----EKEKPRDVPCNNH-SPTTHPEA	944

RESULT 13

TM16A\_HUMAN

ID	TM16A_HUMAN	Reviewed;	986 AA.
AC	Q5XXA6; Q8IYY8; Q8N7V3;		
DT	29-MAY-2007,	integrated into UniProtKB/Swiss-Prot.	
DT	23-NOV-2004,	sequence version 1.	
DT	21-AUG-2007,	entry version 18.	
DE	Transmembrane protein 16A (Discovered on gastrointestinal stromal		
DE	tumors protein 1) (Oral cancer overexpressed protein 2) (Tumor		

DE amplified and overexpressed sequence 2).

GN Name=TMEM16A; Synonyms=DOG1, ORAOV2, TAOS2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.

RX PubMed=16906560; DOI=10.1002/gcc.20371;

RA Huang X., Godfrey T.E., Gooding W.E., McCarty K.S. Jr., Gollin S.M.;

RT "Comprehensive genome and transcriptome analysis of the 11q13 amplicon

RT in human oral cancer and syntenic to the 7F5 amplicon in murine oral

RT carcinoma.";

RL Genes Chromosomes Cancer 45:1058-1069(2006).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).

RC TISSUE=Testis;

RX PubMed=14702039; DOI=10.1038/ng1285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,

RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

RT "Complete sequencing and characterization of 21,243 full-length human

RT cDNAs.";

RL Nat. Genet. 36:40-45(2004).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).

RC TISSUE=Testis;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

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RT      "The status, quality, and expansion of the NIH full-length cDNA
RT      project: the Mammalian Gene Collection (MGC).";
RL      Genome Res. 14:2121-2127(2004).
RN      [4]
RP      IDENTIFICATION, AND TOPOLOGY.
RX      PubMed=12739008;
RA      Katoh M., Katoh M.;
RT      "FLJ10261 gene, located within the CCND1-EMS1 locus on human
RT      chromosome 11q13, encodes the eight-transmembrane protein homologous
RT      to C12orf3, C11orf25 and FLJ34272 gene products.";
RL      Int. J. Oncol. 22:1375-1381(2003).
RN      [5]
RP      SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX      PubMed=15215166;
RA      West R.B., Corless C.L., Chen X., Rubin B.P., Subramanian S.,
RA      Montgomery K., Zhu S., Ball C.A., Nielsen T.O., Patel R.,
RA      Goldblum J.R., Brown P.O., Heinrich M.C., van de Rijn M.;
RT      "The novel marker, DOG1, is expressed ubiquitously in gastrointestinal
RT      stromal tumors irrespective of KIT or PDGFRA mutation status.";
RL      Am. J. Pathol. 165:107-113(2004).
RN      [6]
RP      SUBCELLULAR LOCATION.
RX      PubMed=16261155; DOI=10.1038/sj.onc.1209203;
RA      Carles A., Millon R., Cromer A., Ganguli G., Lemaire F., Young J.,
RA      Wasylyk C., Muller D., Schultz I., Rabouel Y., Dembele D., Zhao C.,
RA      Marchal P., Ducray C., Bracco L., Abecassis J., Poch O., Wasylyk B.;
RT      "Head and neck squamous cell carcinoma transcriptome analysis by
RT      comprehensive validated differential display.";
RL      Oncogene 25:1821-1831(2006).
CC      -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein.
CC      Cytoplasm.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1;
CC      IsoId=Q5XXA6-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q5XXA6-2; Sequence=VSP_025665, VSP_025668, VSP_025669;
CC      Note=No experimental confirmation available;
CC      Name=3;
CC      IsoId=Q5XXA6-3; Sequence=VSP_025666, VSP_025667, VSP_025668,
CC      VSP_025669, VSP_025670, VSP_025671;
CC      Note=No experimental confirmation available;
CC      -!- TISSUE SPECIFICITY: Broadly expressed with higher levels in liver
CC      and skeletal muscle.
CC      -!- SIMILARITY: Belongs to the TMEM16 family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY728143; AAU82085.1; -; mRNA.
DR      EMBL; AK097619; BAC05123.1; -; mRNA.
DR      EMBL; BC033036; AAH33036.2; -; mRNA.
DR      UniGene; Hs.503074; -.
DR      Ensembl; ENSG00000131620; Homo sapiens.
DR      HGNC; HGNC:21625; TMEM16A.
DR      MIM; 610108; gene.

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DR PharmGKB; PA128394678; -.

DR ArrayExpress; Q5XXA6; -.

DR InterPro; IPR007632; DUF590.

DR PANTHER; PTHR12308; DUF590; 2.

DR Pfam; PF04547; DUF590; 1.

PE 1: Evidence at protein level;

KW Alternative splicing; Cytoplasm; Glycoprotein; Membrane; Polymorphism;

KW Transmembrane.

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FT	TOPO_DOM	1	333	Cytoplasmic (Potential).
FT	TRANSMEM	334	354	Potential.
FT	TOPO_DOM	355	402	Extracellular (Potential).
FT	TRANSMEM	403	423	Potential.
FT	TOPO_DOM	424	519	Cytoplasmic (Potential).
FT	TRANSMEM	520	540	Potential.
FT	TOPO_DOM	541	565	Extracellular (Potential).
FT	TRANSMEM	566	586	Potential.
FT	TOPO_DOM	587	606	Cytoplasmic (Potential).
FT	TRANSMEM	607	627	Potential.
FT	TOPO_DOM	628	731	Extracellular (Potential).
FT	TRANSMEM	732	752	Potential.
FT	TOPO_DOM	753	791	Cytoplasmic (Potential).
FT	TRANSMEM	792	812	Potential.
FT	TOPO_DOM	813	882	Extracellular (Potential).
FT	TRANSMEM	883	903	Potential.
FT	TOPO_DOM	904	986	Cytoplasmic (Potential).
FT	CARBOHYD	832	832	N-linked (GlcNAc. . .) (Potential).
FT	VAR_SEQ	1	116	Missing (in isoform 2).
FT				/FTId=VSP_025665.
FT	VAR_SEQ	1	28	Missing (in isoform 3).
FT				/FTId=VSP_025666.
FT	VAR_SEQ	29	36	GYLPSEGT -> MLTRPSQV (in isoform 3).
FT				/FTId=VSP_025667.
FT	VAR_SEQ	448	451	Missing (in isoform 2 and isoform 3).
FT				/FTId=VSP_025668.
FT	VAR_SEQ	476	501	Missing (in isoform 2 and isoform 3).
FT				/FTId=VSP_025669.
FT	VAR_SEQ	651	700	CAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIR
FT				YLKLKQQSP -> VTEILFISGSPFCLAYDLSTPCTWEKQL
FT				QHICSAKSSRFLSFLLETFLFP (in isoform 3).
FT				/FTId=VSP_025670.
FT	VAR_SEQ	701	986	Missing (in isoform 3).
FT				/FTId=VSP_025671.
FT	VARIANT	608	608	F -> S (in dbSNP:rs2186797).
FT				/FTId=VAR_032417.
FT	VARIANT	983	983	G -> R (in dbSNP:rs3740722).
FT				/FTId=VAR_032418.
FT	CONFLICT	801	801	N -> D (in Ref. 3; AAH33036).
FT	CONFLICT	948	948	W -> C (in Ref. 3; AAH33036).
SQ	SEQUENCE	986 AA;	114078 MW;	E30A02F91EF36FC2 CRC64;

Query Match 35.2%; Score 1450.5; DB 1; Length 986;

Best Local Similarity 39.1%; Pred. No. 7.1e-112;

Matches 335; Conservative 149; Mismatches 255; Indels 117; Gaps 24;

Qy	5	QDGNTTVH---YALLSASWAVLCYYAEDLRKLPLQELPNQASNWSAGLLAWLGIPNVLL	61
Db	144	RDEDTKIHGVGVFKIHAPWNVLCREAEFLKLKMP TKKMYH--INETRGLLK--KINSVLQ	199
Qy	62	EVVPDVPPEYYSCR-----FRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	111
Db	200	KITDPIQPKVAEHRPQTMKRLSYFPSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTT	258
Qy	112	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN	171
Db	259	CTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEFNDRKLLYEEWARYGVFY	312
Qy	172	KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	231
Db	313	KYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQ	372
Qy	232	KDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLLEYWKRKSA	290
Db	373	RHNITMCPLCDKTC SYWKMSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQM	432
Qy	291	TLAYRWDCSDYEDTEE----RPRPQFAA-----SAPMTAPNPITGEDEPYFPERS-----	336
Db	433	RLNYRWDLTGFEETEEAVKDHPRAEYEARVLEKSLKKESRNK---EKRRHIPEESTNKWK	489
Qy	337	-RARRMLAG-----SVVIVVMVAVVVMCLVSIILYRAIMAIIVVS	374
Db	490	QRVKTAMAGVKLTDKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIIYRISMAAALA	549
Qy	375	RSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLK	434
Db	550	MNSSPSVRSNIRVTVTATAVIINLVVILLDEVYGC IARWLTKIEVPKTEKSFEERLIFK	609
Qy	435	VFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMV	493
Db	610	AFLKLFVNSYTPIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIML	669
Qy	494	GKQVI-NNMQEVLI PKLKGWWQKFR LRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEY	552
Db	670	GKQLIQNNLFEIGIPKMKKLIRYLKLKQQSPDHEECV KRKQRYEVDYNLEPFAGLTPEY	729
Qy	553	LEMVLQFGFVTIFVAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHI	612
Db	730	MEMIIQFGFVTLFVASFPLAPL FALLNNIIEIRLDAKKFVTELRRPVAVRAKDIGIWYNI	789
Qy	613	LAGLTHLAVISNAFLLAFSSDFLPRA--YYRWTRAHDLRGFLNFTLARAPSSF-----	663
Db	790	LRGIGKLAVIINAFVISFTSDFIPRLVLYMYSKNGTMMHGFVNHTL---SSFNVSDFQN	845
Qy	664	AAAHN-----RTCRYRAFRD---DDGHY--SQT YWNLLAIRLAFVIVFEHVVSFVG	709
Db	846	GTAPNDPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLVMFMS	905
Qy	710	RLDLLVLPDIPESVEIKVKREYYLA-----KQALAENEVLFGTNGTKDEQP----	755
Db	906	DFVDWVIPDIPKDISQIHKVKVLMVELFMREEQDKQQLL--ETWMEKERQKDEPPCNHH	963

Qy 756 -----KGSELSSH 763  
|| ||  
Db 964 NTKACPDSLGGSPAPSH 979

## RESULT 14

## TM16B\_HUMAN

ID TM16B\_HUMAN Reviewed; 999 AA.  
AC Q9NQ90;  
DT 16-JAN-2004, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-2000, sequence version 1.  
DT 24-JUL-2007, entry version 35.  
DE Transmembrane protein 16B.  
GN Name=TMEM16B; Synonyms=C12orf3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Retina;  
RA Lorenz B., White K.E., Econs M.J., Strom T.M.;  
RT "Transcripts in 12p13.3.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.  
CC -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein  
CC (Probable).  
CC -!- SIMILARITY: Belongs to the TMEM16 family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AJ272204; CAC01125.1; -; mRNA.  
DR UniGene; Hs.148970; -.  
DR Ensembl; ENSG00000047617; Homo sapiens.  
DR KEGG; hsa:57101; -.  
DR HGNC; HGNC:1183; TMEM16B.  
DR MIM; 610109; gene.  
DR PharmGKB; PA25504; -.  
DR LinkHub; Q9NQ90; -.  
DR ArrayExpress; Q9NQ90; -.  
DR GermOnline; ENSG00000047617; Homo sapiens.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
KW Membrane; Polymorphism; Transmembrane.  
FT CHAIN 1 999 Transmembrane protein 16B.  
FT /FTId=PRO\_0000072564.  
FT TRANSMEM 360 382 Potential.  
FT TRANSMEM 535 557 Potential.  
FT TRANSMEM 577 599 Potential.  
FT TRANSMEM 619 641 Potential.  
FT TRANSMEM 746 768 Potential.

FT	TRANSMEM	796	818	Potential.
FT	TRANSMEM	898	920	Potential.
FT	VARIANT	108	108	V -> A (in dbSNP:rs3741903).
FT				/FTId=VAR_021932.
FT	VARIANT	501	501	S -> A (in dbSNP:rs1860961).
FT				/FTId=VAR_020331.
SQ	SEQUENCE	999 AA;	113616 MW;	B9B4F56161AE1B00 CRC64;

Query Match 34.9%; Score 1437; DB 1; Length 999;  
 Best Local Similarity 38.7%; Pred. No. 9.8e-111;  
 Matches 326; Conservative 161; Mismatches 263; Indels 92; Gaps 23;

Qy	1	QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQ-----ASNWSAGLLAW	53
		: ::: : :             : : :  : : :   :	
Db	170	EKDLENKSQGSIFVRIHAPWQVLAREAEFLKIKVPTKKEMYEIKAGGSIKKFSAAAL---	226
Qy	54	LGIPNVLLEVPDPPEYYSCRFRVNKL-----RFLGSDNQDTFFTSTKRHQILFEIL	107
		: :       : : : :   :      :   :  :	
Db	227	---QKLSSHLQPRV-PEHSNNKMKNLSYPFSREKMYLYNIQEKDTFFDNATRSRIVHEIL	282
Qy	108	AKTPYGHEKKNLLGIHQLLAEGVLSAAFP LHDGPFKTPPEGPQAPRLNQRQVLFQHWARW	167
		:  :	
Db	283	KRTACS-RANNTMGINS LIANNIYEAA YPLHDGEYDSPEDD-----MNDRKLLYQEWARY	336
Qy	168	GKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGT LVFLVGCFLVFSDIPTQE	227
		:   :	
Db	337	GVFYKFQPIDLIRKYFGEKIGLYFAWLGLYTSFLIPSSVIGVIVFLYGCATIEEDIPSRE	396
Qy	228	LCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWK	286
		:  : : :            :  :  :  :  :  :  :  :  :  :  :  :  :  :	
Db	397	MCDQQNAFTMCPLCDKSCDYWNLSACGTAQASHLFDNPATVFFSIFMALWATMFLENWK	456
Qy	287	RKSATLAYRWDCSDYEDTEER----PRPQFAA-----SAPMTAPNPIT----G	326
		:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :	
Db	457	RLQMRLGYFWDLTGIEEEEEERAQEHRSPEYETKVREKMLKESNQSAVQKLETNTTECGDE	516
Qy	327	EDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWAS	386
		:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :	
Db	517	DDEDKLTWKDRFPGYLMNFASILFMIALTFSIVFGVIVYRITTAALS-----LNKATRS	571
Qy	387	RI---ASLTGSVNLVFILILSKIYVSLAHVLRWEMHRTQTKFEDAFTLKVFIFQFVNF	443
		: :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :	
Db	572	NVRVTVTATAVIINLVVILILDEIYGAVAKWLTKIEVPKTEQTFEERLILKAFL LKFVNA	631
Qy	444	YSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNM	501
		:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :	
Db	632	YSPIFYVAFFKGRFVGRPGSYVYVFDGYRMEECAPGGCLMELCIQLSIIMLGKQLIQNNI	691
Qy	502	QEV LIPKLKGWWQKFR LRSKKRKAGASAGA-SQGP--WEDDYELVPCEGLFDEYLEMVLQ	558
		: :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :	
Db	692	FEIGV PKLK---KLFRKLKDETEAGETDSAHSKHPEQWDL DYSLEPYTGLTPEYMEMIIQ	748
Qy	559	FGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH	618
		:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :	
Db	749	FGFVT L FVASFPLAPVFALLNNVIEVRLDAKKFVTELRRPDAVRTKDIGIWF DILSGIGK	808

Qy 619 LAVISNAFLFLAFSSDFLPRAYRWTRAHD--LRGFLNFTLA-----RAPSSFAA 665  
:|||||::| :||:| |::: |: | |:| |: : :|  
Db 809 FSVISNAFVIAITSDFIPRLVYQYSYSHNGTLHGfVNHTLSFFNVSQlKEGTQPENSQFD 868  
  
Qy 666 AHNRTCryRAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEHVVSvGRLLDLLVPDIP 720  
: ||:: |: : :|: || |:| |||||:|::| : |:| ::|||  
Db 869 QEVQFCRFKDYREPPWAPNPYEFskQYWFILSARLAFVlIFQNLVMFLSVLVDWMIPDIP 928  
  
Qy 721 ESVEIKVKRE-----YYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKA-S 773  
: ::|:| :|: | :| | : | | : | : | |  
Db 929 TDISDQIKKEKSLLVDFFLKE----EHEKLKLMDEPALRSPGGGDRSRsRAASSAPSGQS 984  
  
Qy 774 QL 775  
||  
Db 985 QL 986

RESULT 15

Q8CFW1\_MOUSE

ID Q8CFW1\_MOUSE Unreviewed; 913 AA.  
AC Q8CFW1;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 24-JUL-2007, entry version 21.  
DE Transmembrane protein 16B.  
GN Name=Tmem16b;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Query Match 34.8%; Score 1434.5; DB 2; Length 913;  
Best Local Similarity 39.5%; Pred. No. 1.4e-110;  
Matches 310; Conservative 160; Mismatches 242; Indels 73; Gaps 18;

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Qy	446	SPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQE	503
		:          :               :   :   :     :     :	
Db	547	PIFYVAFFKGRFVGRPGSYVYVFDGYRMEECAPGGCLMELCIQLSIIMLGKQLIQNNIFE	606
Qy	504	VLIPKLKGWWQKFRLRSKRRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVT	563
		: :         : :   : : : : :   :   :           :   :   :	
Db	607	IGVPKLKKLFRKLKDETEPGESDPDHSKRPEQWDLDSLEPYTGLTPEYMEMIIQFGFVT	666
Qy	564	IFVAACPLAPLFPALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVIS	623
		:       :       :         :   :       :           :	
Db	667	LFVASFPLAPVFALLNNVIEVRLDAKKFVTELRRPDAVRTKDIGIWFIDILSGIGKFSVII	726
Qy	624	NAFLAFSSDFLPRAYYRWTRAHD--LRGFLNFTLA-----RAPSSFAAAHNRT	670
		: :   :     :     : : :   :     :     : : :   : :   : :	
Db	727	NAFVIAVTSDFIPLRVYQYSYSHNGTLHGFFVNHTLSFFNVSQLKEGTQPEMSQFDQEVQF	786
Qy	671	CRYRAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDIPESVEI	725
		: : :   : : : :   : :           :   : :   : :   :   : :       :	
Db	787	CRFKDYREPPWAPNPYEFQYWSVLSARLAFVIFQNLVMFLSVLVDWMIPDIPTDISD	846
Qy	726	KVKRE	730
		: :   :	
Db	847	QIKKE	851

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Job time : 538 secs

SCORE 3.3